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The new GeneChip® One-Cycle and Two-Cycle cDNA Synthesis Kits.


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Full Record

Details for HUGENEFL:X15880_AT

Full Screen

NetAffx Links [Cluster Members](#)
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GeneChip Array Information

Probe Set ID X15880_at
GeneChip Array HumanGeneFL Array
Organism Common Name Human

Probe Design Information

Transcript ID X15880
Sequence Type Exemplar sequence
Representative Public ID X15880 [NCBI](#)
Target Description X15880, class C, 20 probes, 20 in all_X15880 1690-2273, Human mRNA for collagen VI alpha-1 C-terminal globular domain

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)

Alignment(s)	Position	% Identity	Cytoband
chr21: 46280561-46281145 (+)	UCSC	100	q22.3

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_001848 NCBI	collagen, type VI, alpha 1	chr21:46257869-46281164 (+) UCSC

Public Domain and Genome References

Gene Title collagen, type VI, alpha 1
Gene Symbol COL6A1 [HGNC](#)
Chromosomal Location 21q22.3
UniGene ID Hs.415997 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000142156 [Ensembl](#)
LocusLink 1291 [NCBI](#)
SwissProt P12109 [EMBL-EBI](#)
Q7Z645 [EMBL-EBI](#)
Q8TBN2 [EMBL-EBI](#)
Q9BSA8 [EMBL-EBI](#)
OMIM 120220 [NCBI](#)

RefSeq Protein ID NP_001839 NCBI

RefSeq RefSeq Transcript ID RefSeq Title
NM_001848 NCBI collagen, type VI, alpha 1 precursor

Functional Annotations

	ID	Title	Organism	Type
Ortholog	MG-U74AV2:162459_F_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MG-U74AV2:95493_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MOE430A:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MU11KSUBB:X66405_S_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MOUSE430_2:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MOUSE430A_2:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
7155	cell adhesion	non-traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5578	extracellular matrix	inferred from electronic annotation	QuickGO AmiGO
5589	collagen type VI	non-traceable author statement	QuickGO AmiGO

Gene Ontology

GO Molecular Function (view graph)

ID	Description	Evidence	Links
5194	cell adhesion molecule activity	inferred from electronic annotation	QuickGO AmiGO
5201	extracellular matrix structural constituent	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities	Method	ID	Description	E-Value
	blast	15011913		0.0
	blast	13878903		0.0

Protein Domains	Database	ID	Description	E-Value
	scop	d1atza_	d1atza_ SCOP:c.62.1.1: von Willebrand factor A3 domain	3.63E-37
	pfam	vwa	von Willebrand factor type A domain	9.6E-24
	pfam	vwa	von Willebrand factor type A domain	4.7E-32
	pfam	vwa	von Willebrand factor type A domain	2.7E-35
	pfam	Collagen	Collagen triple helix repeat (20 copies)	2.4E-11
	pfam	Collagen	Collagen triple helix repeat (20 copies)	3.8E-14
	pfam	Collagen	Collagen triple helix repeat (20 copies)	3.3E-10
	pfam	Collagen	Collagen triple helix repeat (20 copies)	2.6E-11
	InterPro	IPR008161 EMBL-EBI	Collagen helix repeat	
	InterPro	IPR002035 EMBL-EBI	von Willebrand factor, type A	

InterPro IPR008160 Collagen triple helix repeat
EMBL-EBI

Sequence

Target
Sequence

>HUGENEFL:X15880_AT
agcaagacgcctctcggggcctgtgccgcactagcctccctctcctctgtcccatagct
ggtttttcccaccaatcctcacctaacagttactttacaattaaactcaaagcaagctct
tctcctcagcttggggcagccattggcctctgtctcgttttgggaaaccaagggtcaggag
gccgttgcagacataaatctcggcgactcggcccgctcctgaggggtcctgctggtgac
cggcctggaccttggccctacagccctggaggccgctgctgaccagcactgaccccgacc
tcagagagtactcgcaggggcgctggctgcactcaagaccctcgagattaacgggtgctaa
ccccgtctgctcctcctcccgagagactggggcctggactggacatgagagcccttg
gtgccacagagggtgtgtcttactagaaacaacgcaaacctctccttcctcagaatagt
gatgtgttcgacgttttatcaaaggccccctttctatgttcatgttagttttgctccttc
tgtgtttttttctgaaccatatccatgttgctgacttttccaa

Probe Sequence(5'-3')	Probe		Probe	Strandedness
	X	Y	Interrogation Position	
AGCAAGACGCCTCTCGGGGCCTGTG	76	317	1702	Antisense
AAACTCAAAGCAAGCTCTTCTCCTC	77	317	1804	Antisense
AAAGCAAGCTCTTCTCCTCAGCTTG	78	317	1810	Antisense
TCTCCTCAGCTTGGGGCAGCCATTG	79	317	1822	Antisense
GCCATTGGCCTCTGTCTCGTTTTGG	80	317	1840	Antisense
GCAGACATAAATCTCGGCGACTCGG	81	317	1888	Antisense
GCCCCGTCTCCTGAGGGTCCTGCTG	82	317	1912	Antisense
TGGCCCTACAGCCCTGGAGGCCGCT	83	317	1954	Antisense
TCAGAGAGTACTCGCAGGGGCGCTG	84	317	2002	Antisense
AGTACTCGCAGGGGCGCTGGCTGCA	85	317	2008	Antisense
GGCGCTGGCTGCACTCAAGACCCTC	86	317	2020	Antisense
GGACATGAGAGCCCCTTGGTGCCAC	87	317	2104	Antisense
GAGAGCCCCTTGGTGCCACAGAGGG	88	317	2110	Antisense
CCCTTGGTGCCACAGAGGGCTGTGT	89	317	2116	Antisense
GTGCCACAGAGGGCTGTGTCTTACT	90	317	2122	Antisense
CAGAGGGCTGTGTCTTACTAGAAAC	91	317	2128	Antisense
CTCCTTCCTCAGAATAGTGATGTGT	92	317	2164	Antisense
TTTTTCTGAACCATATCCATGTTGC	93	317	2248	Antisense
TGAACCATATCCATGTTGCTGACTT	94	317	2254	Antisense
ATATCCATGTTGCTGACTTTTCCAA	95	317	2260	Antisense